

FIG. 1

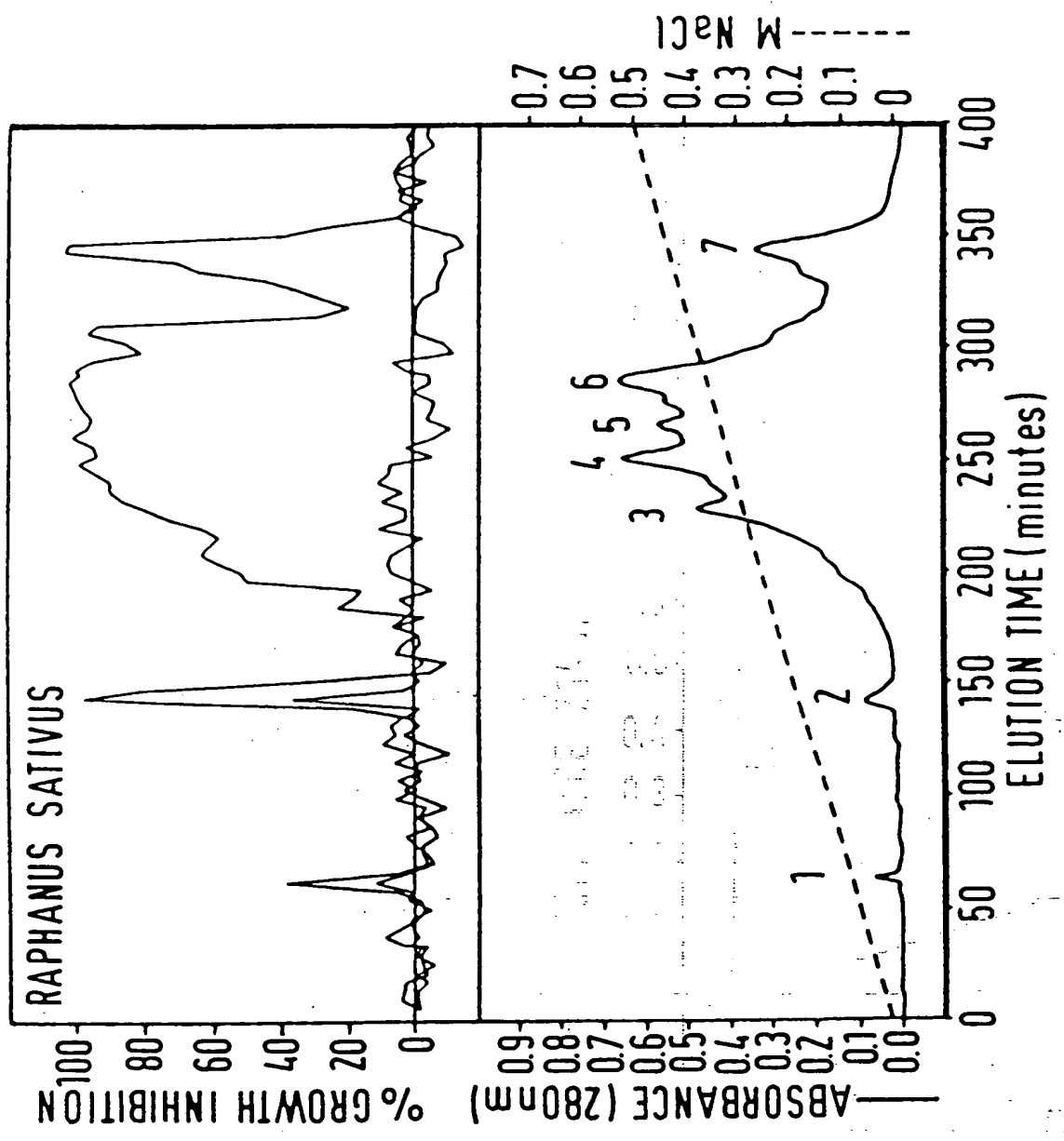


FIG. 2A

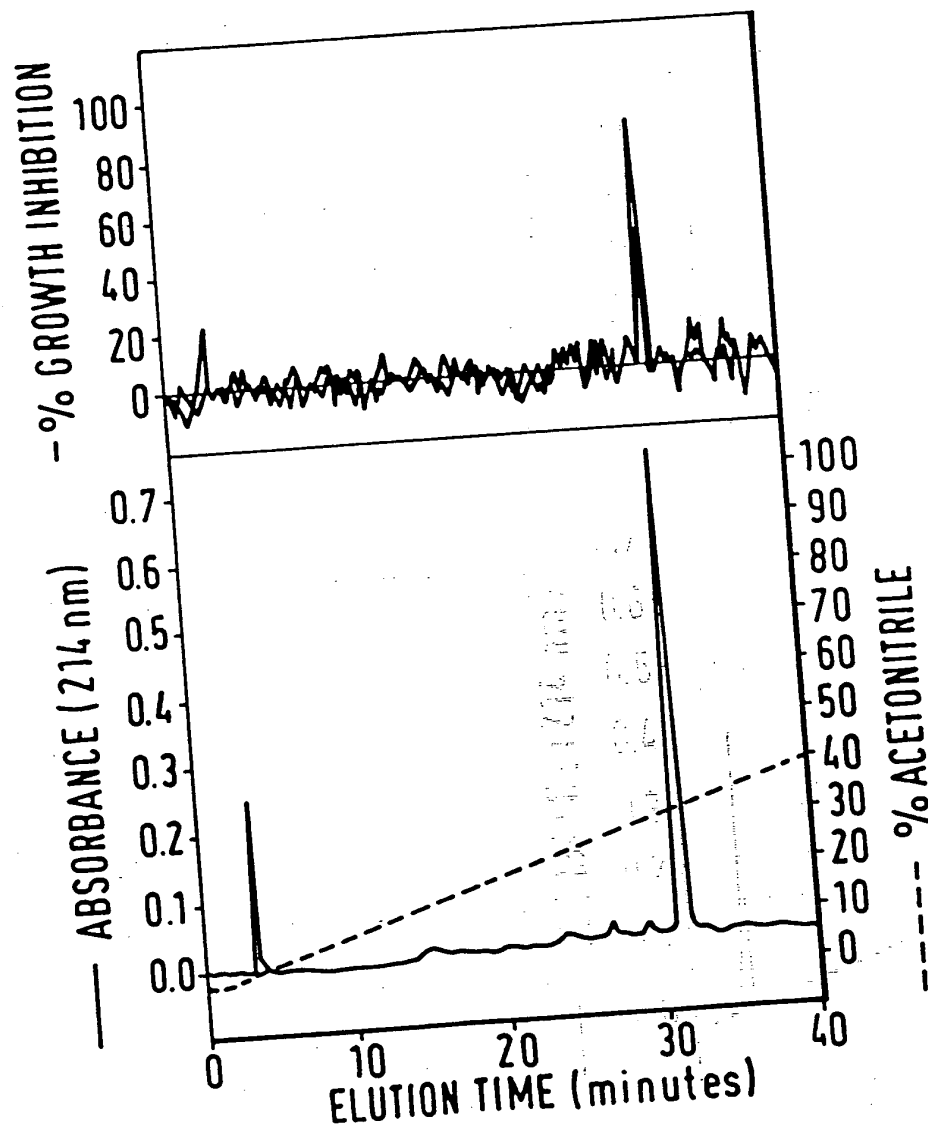


FIG. 2B

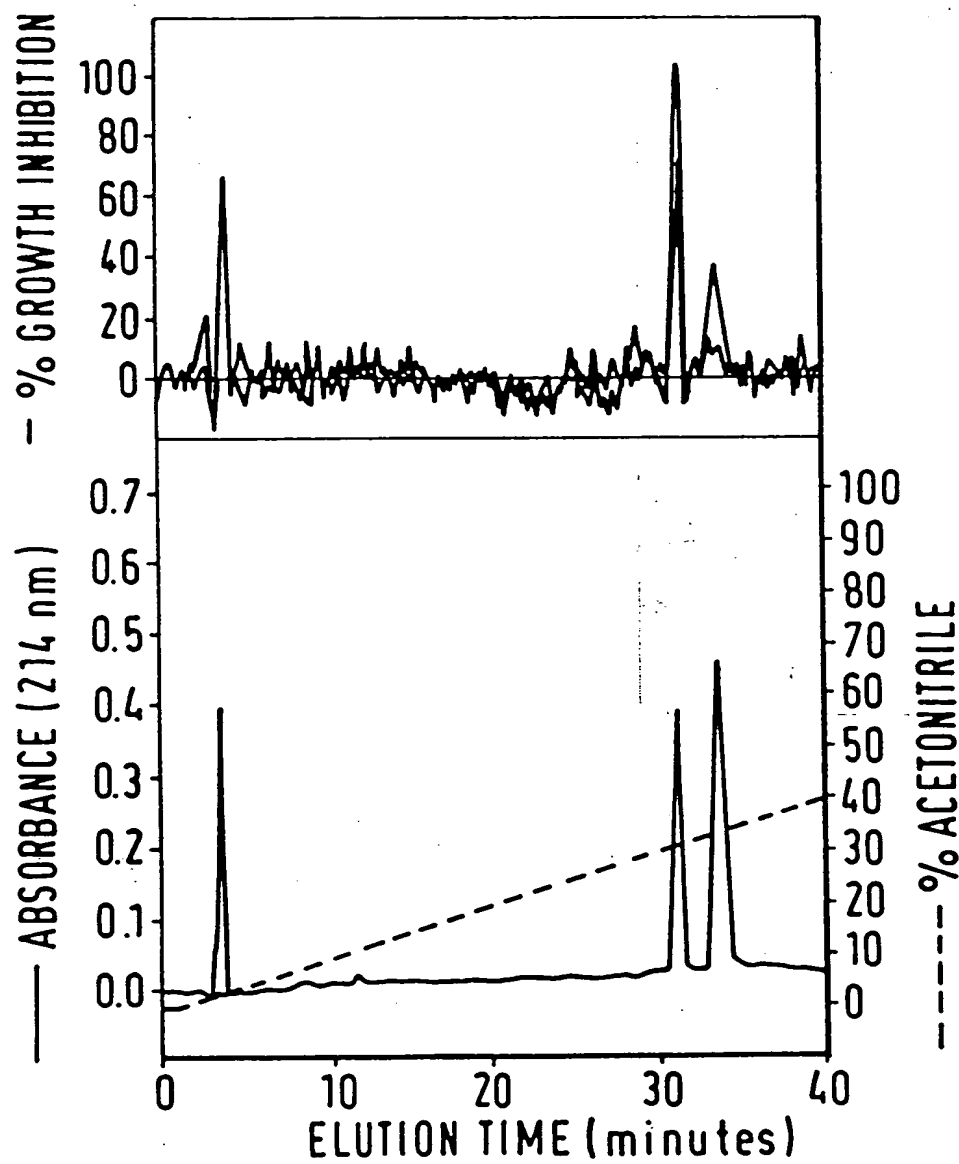
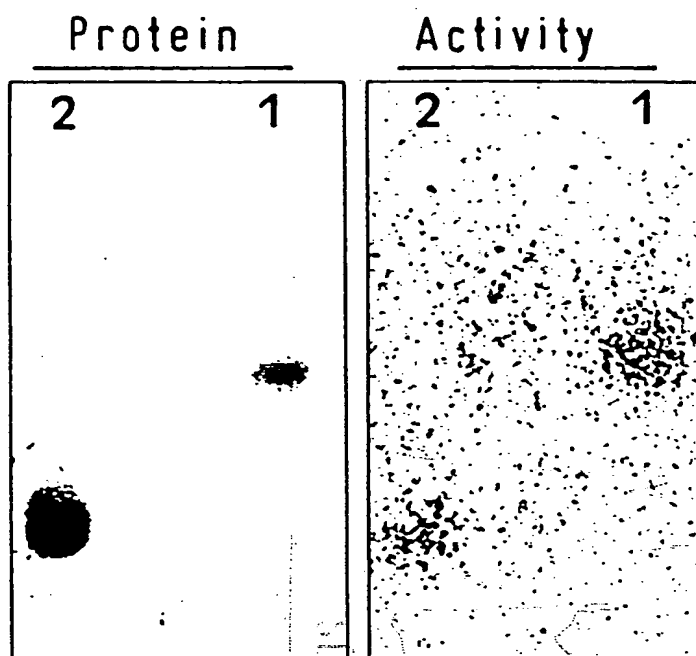


FIG. 3



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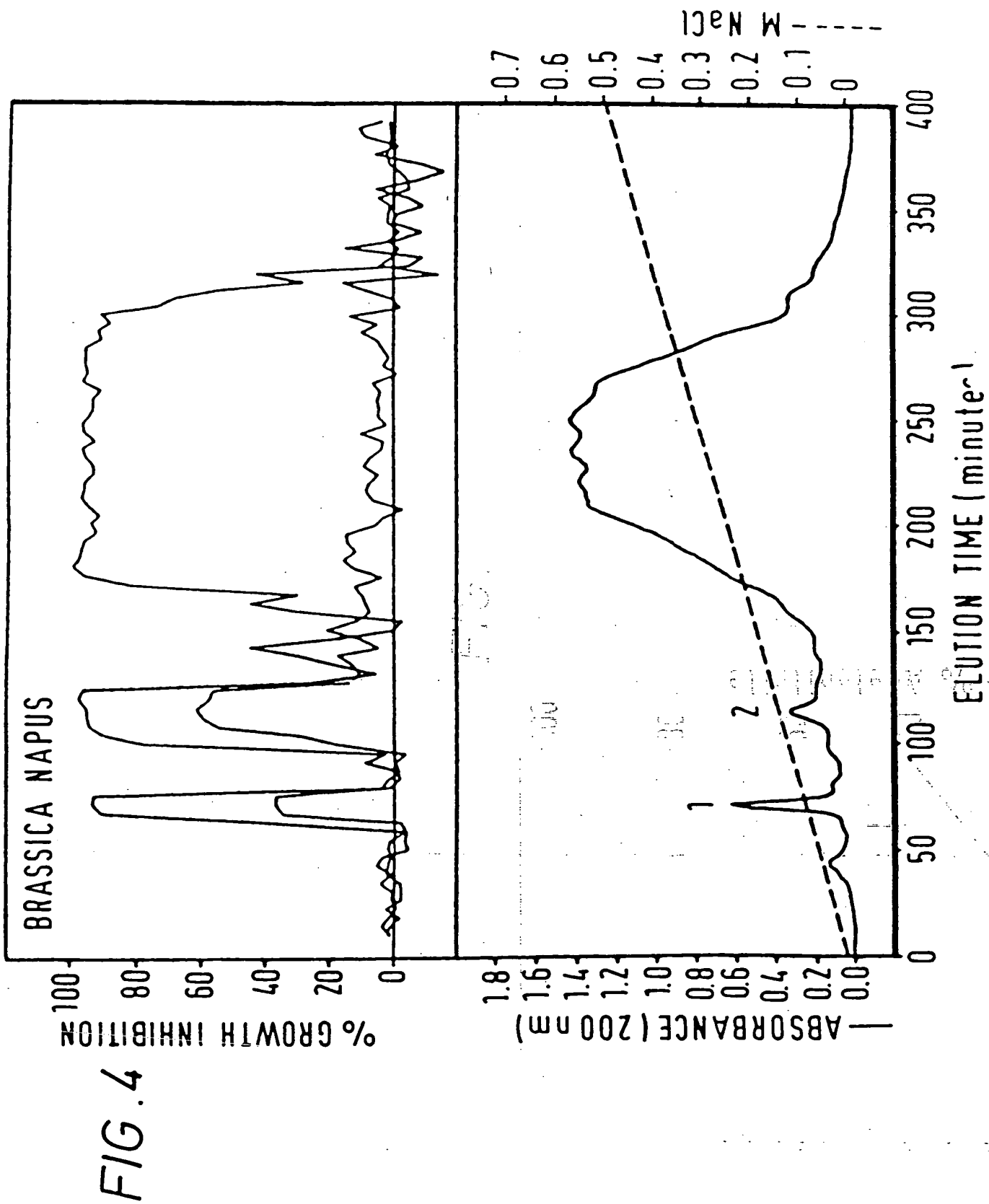
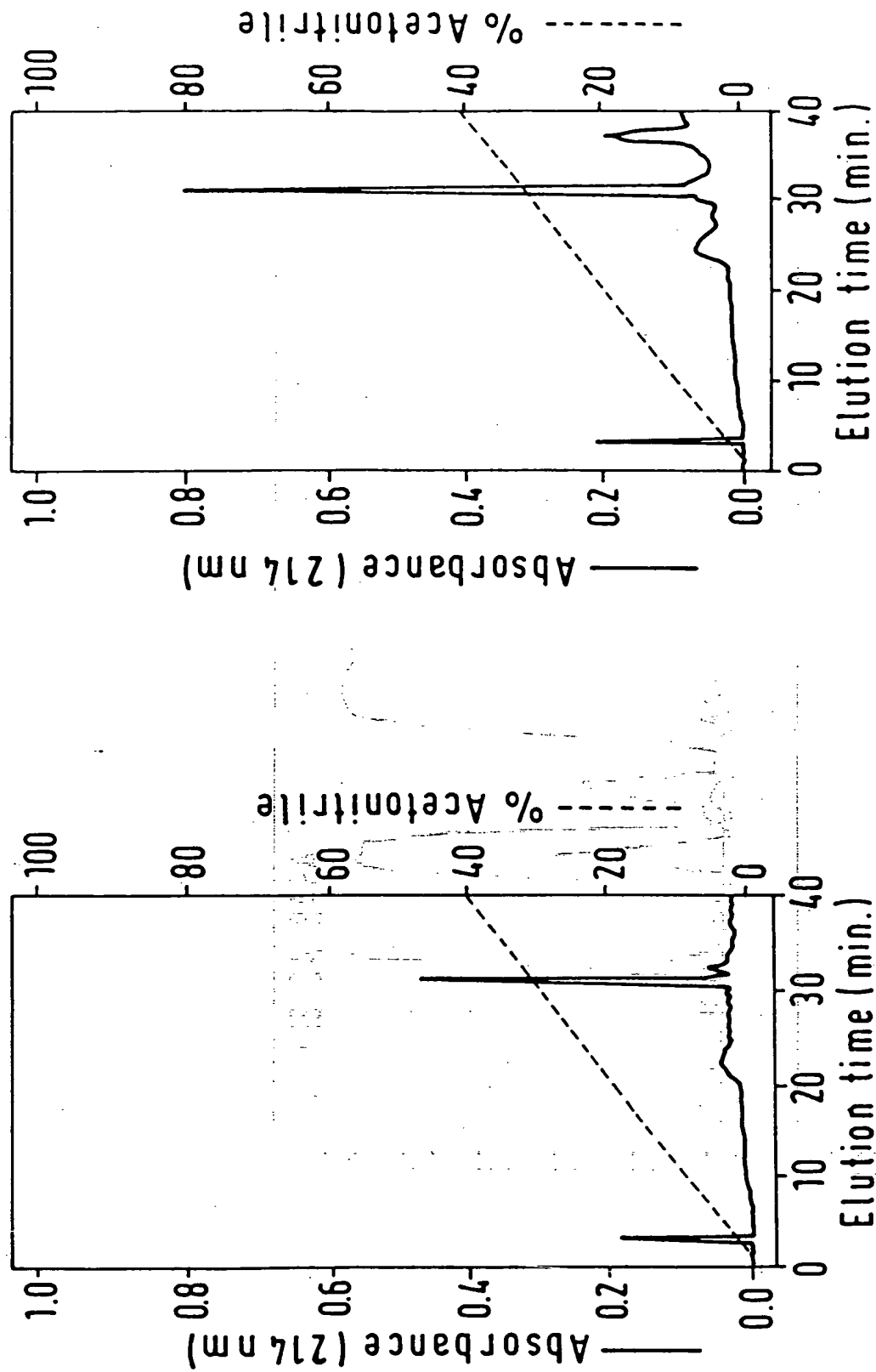


FIG. 5



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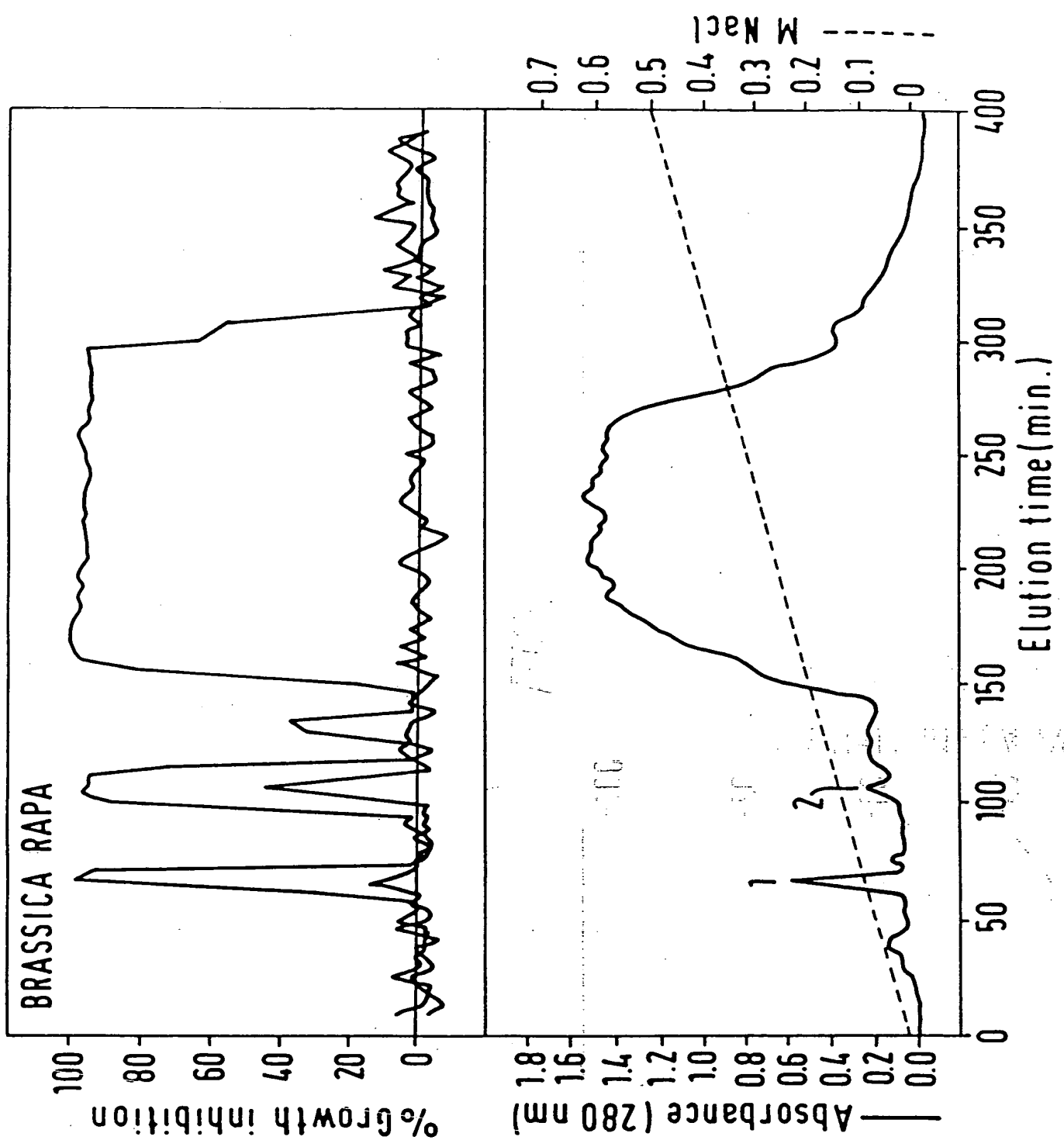
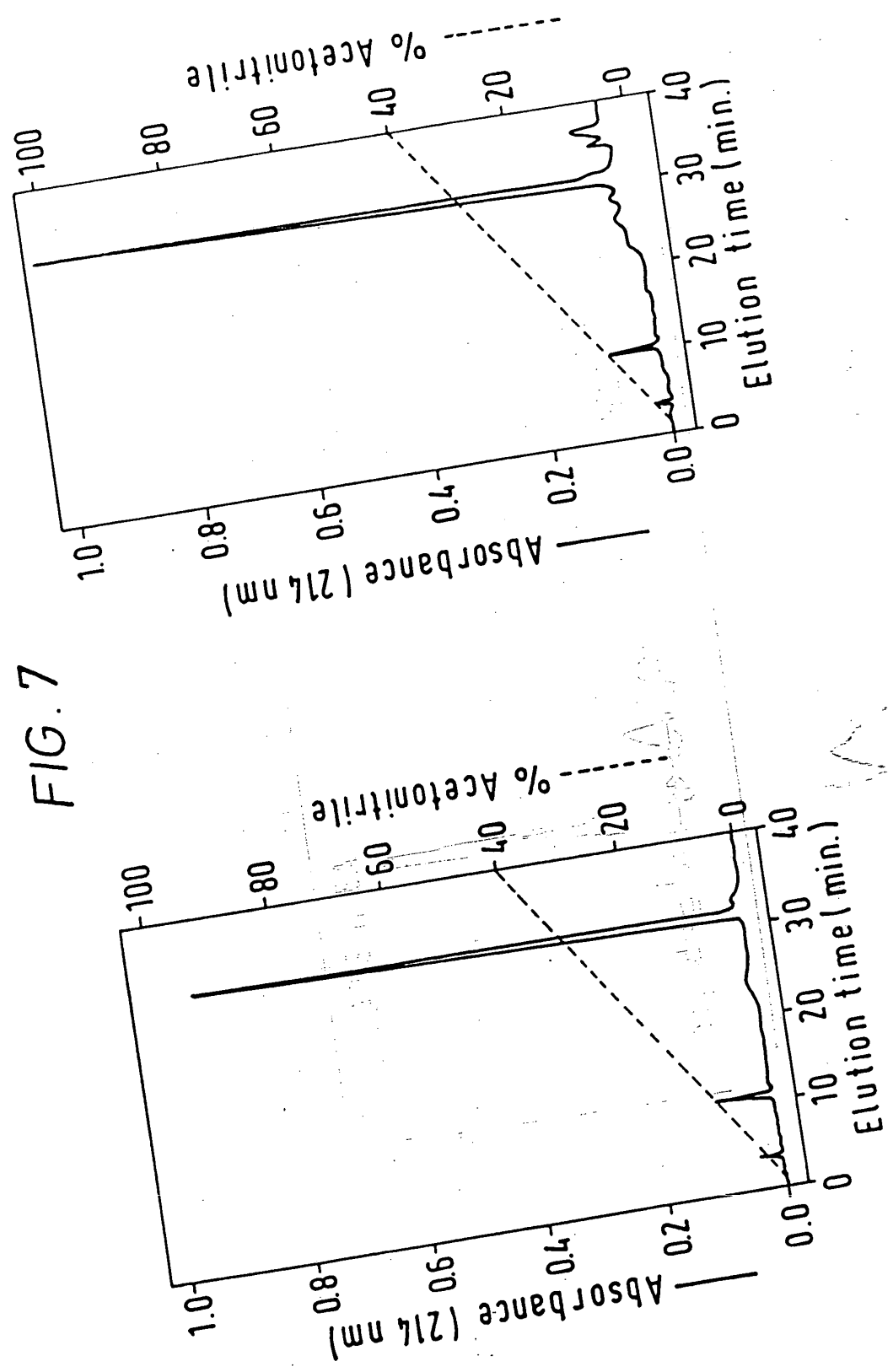


FIG. 6

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FIG. 7



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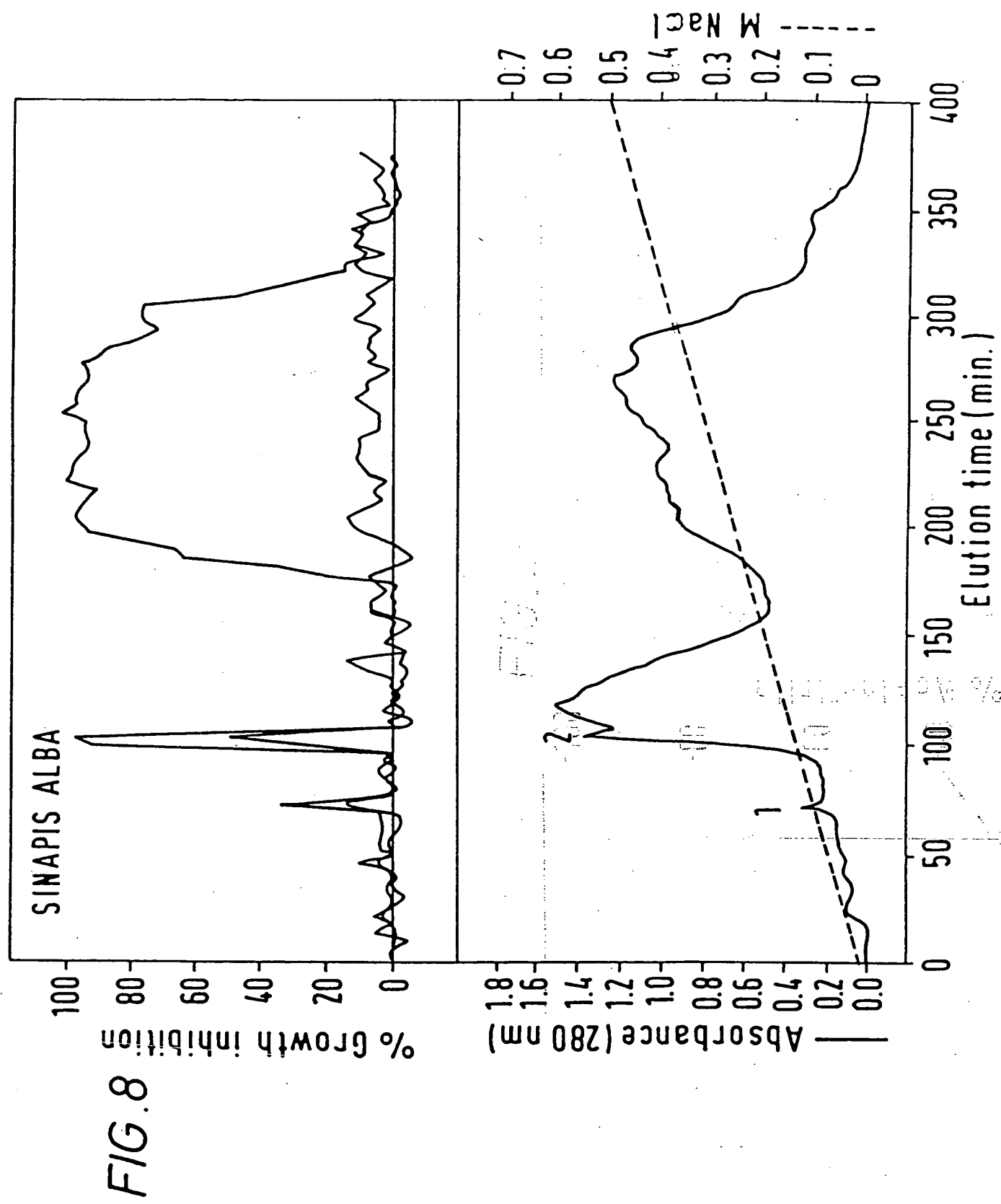


FIG. 9

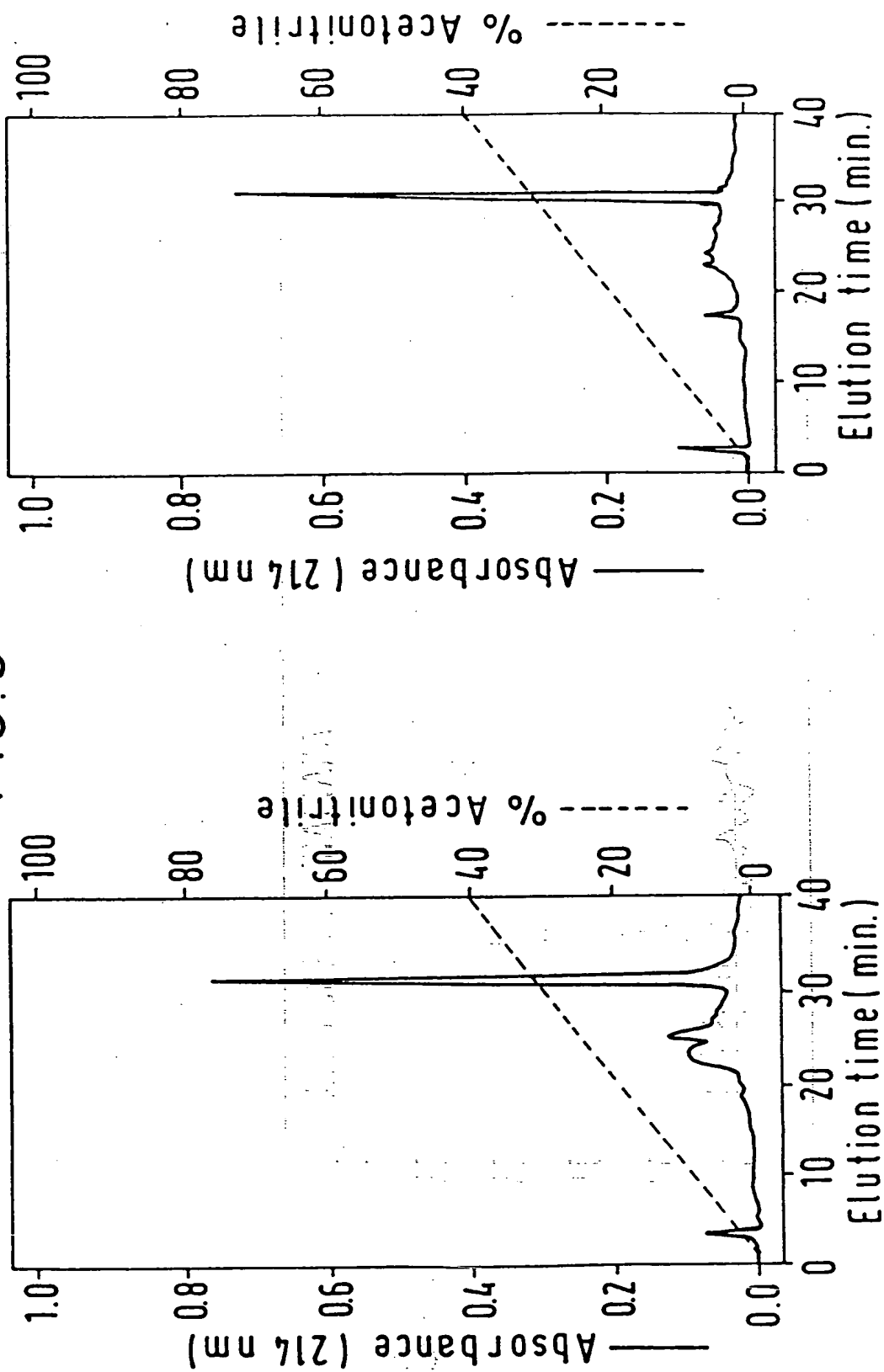


FIG.10

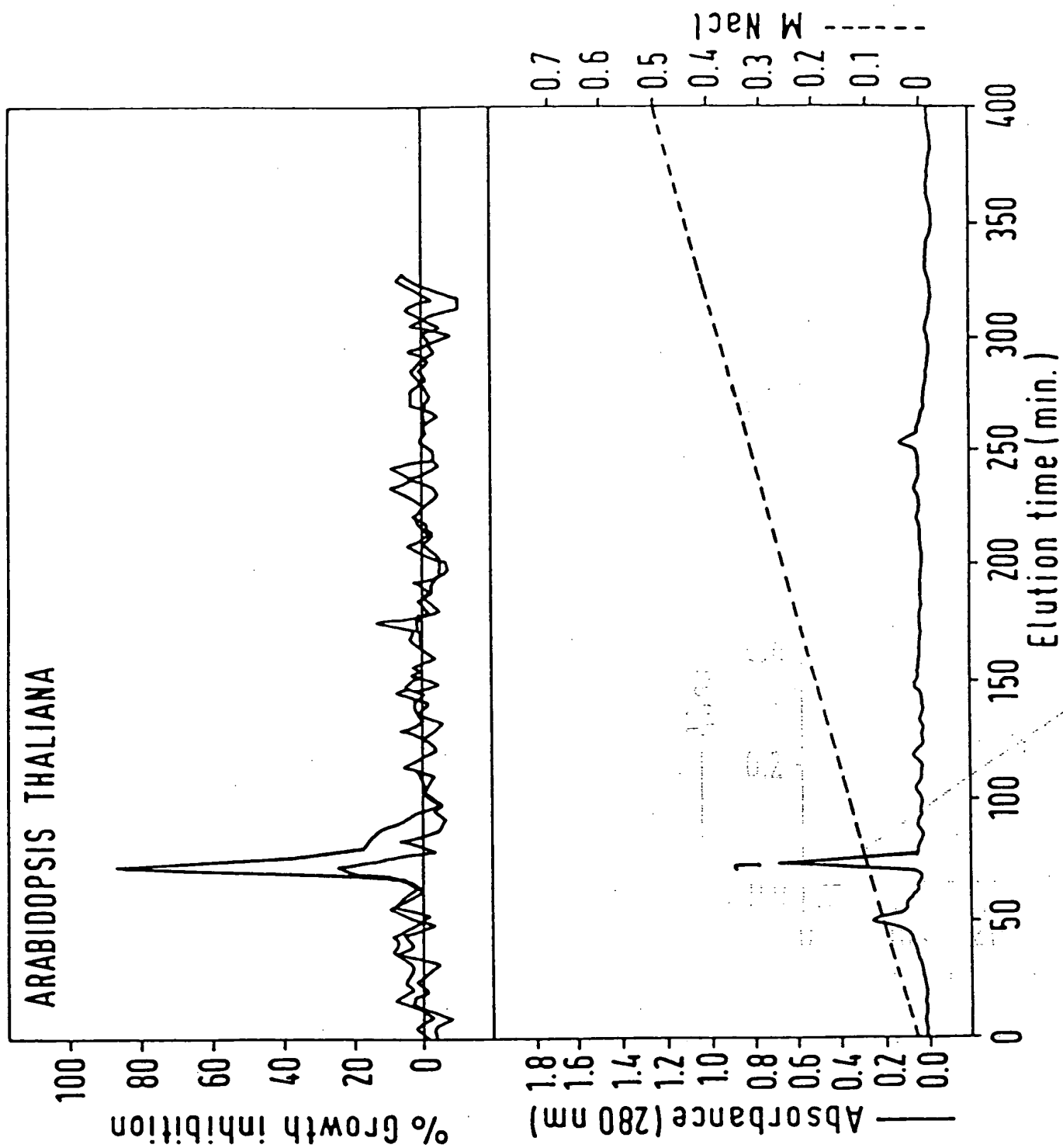


FIG. 11

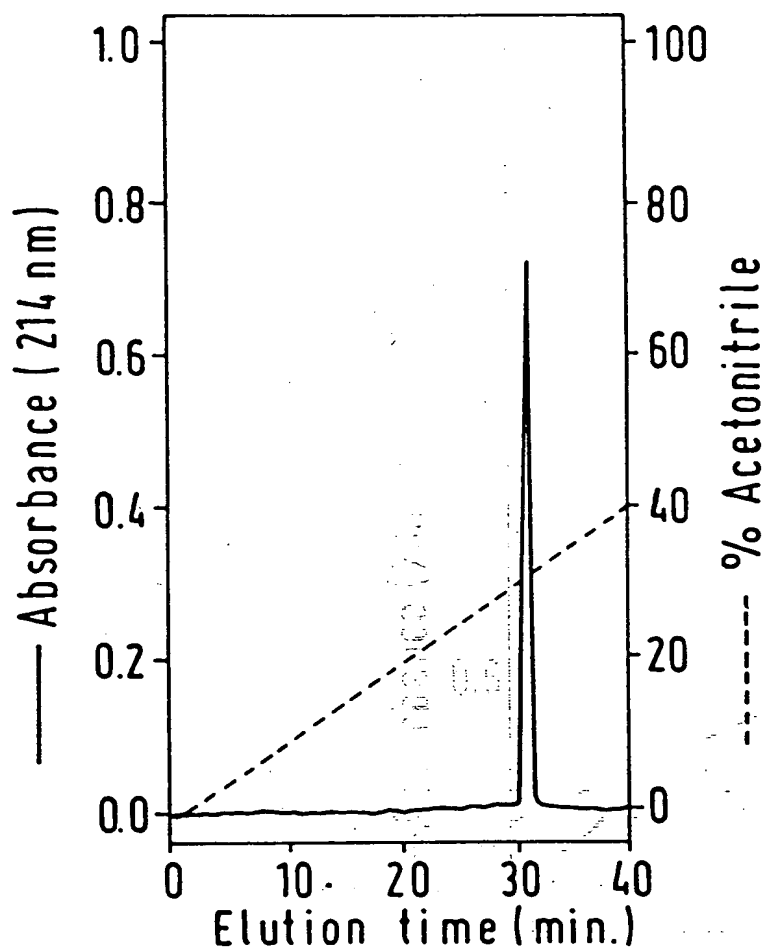


FIG. 12

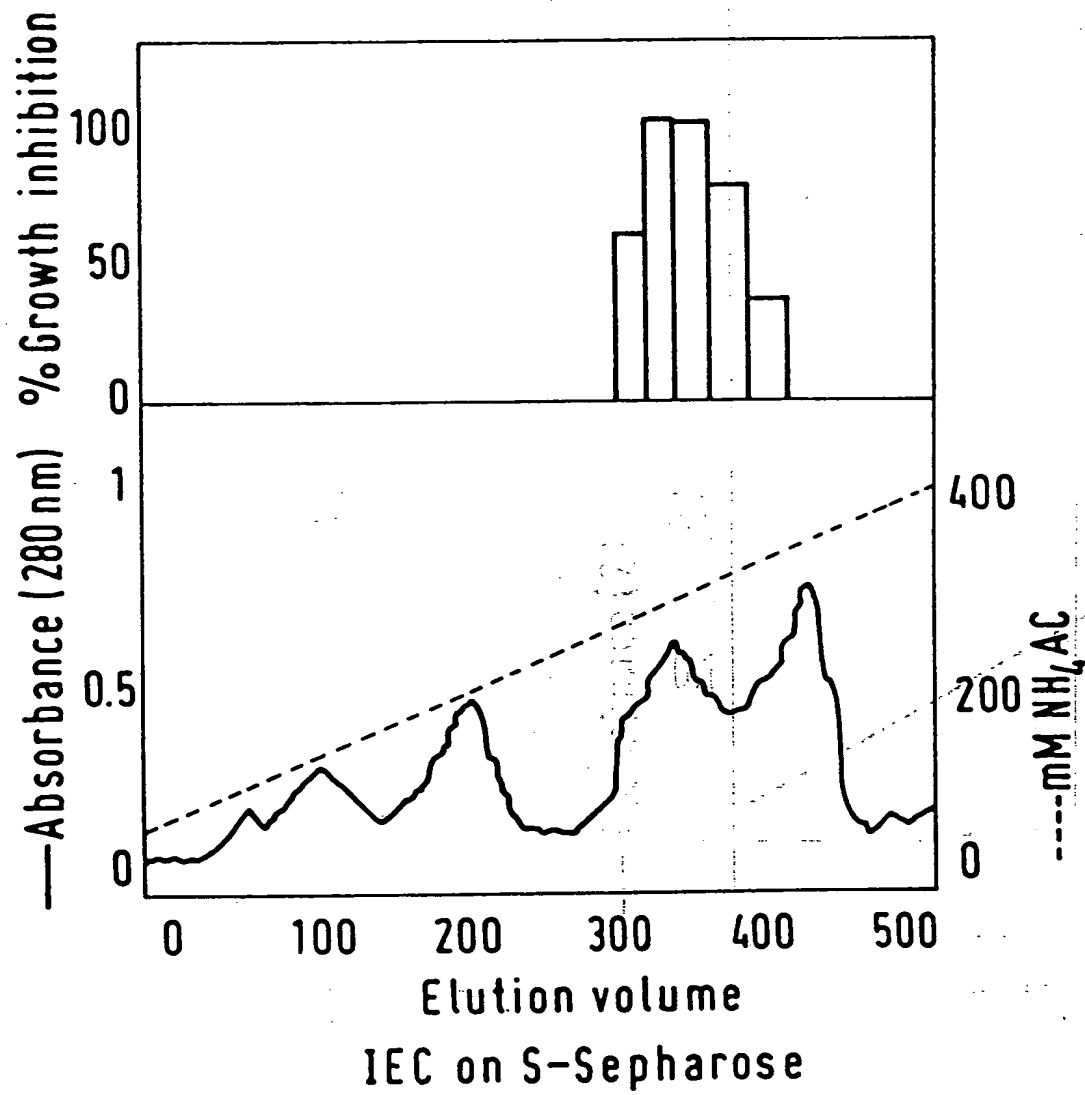


FIG. 13

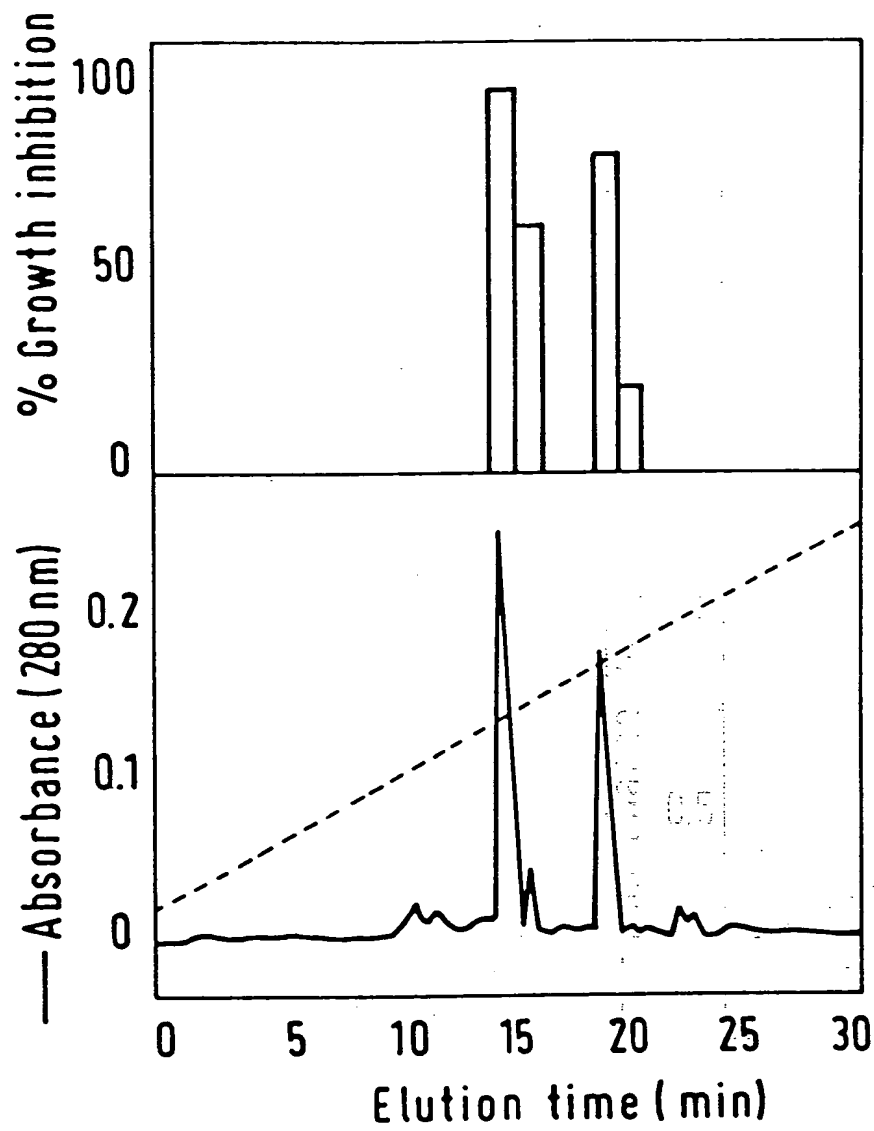


FIG. 14

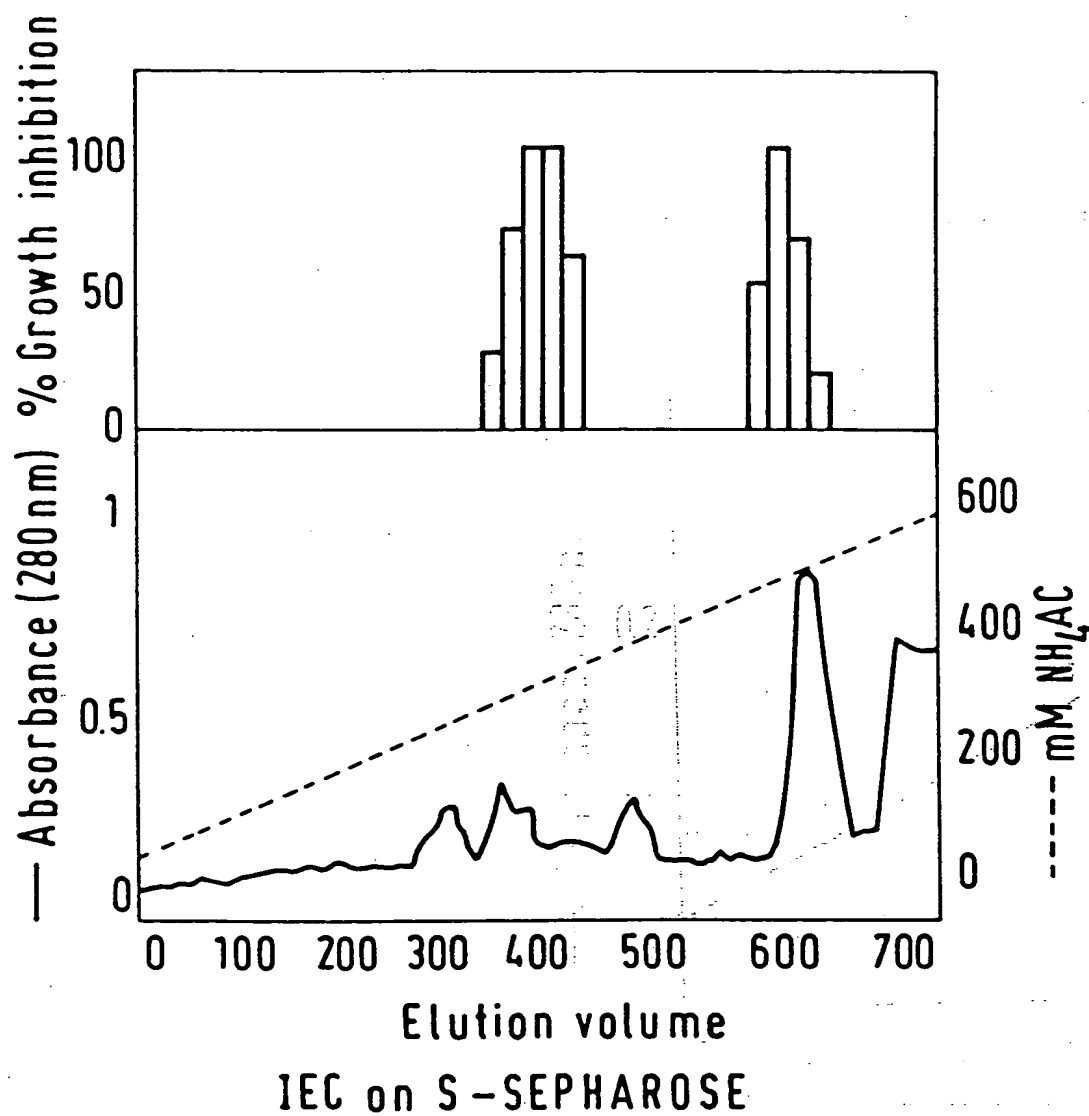


FIG.15

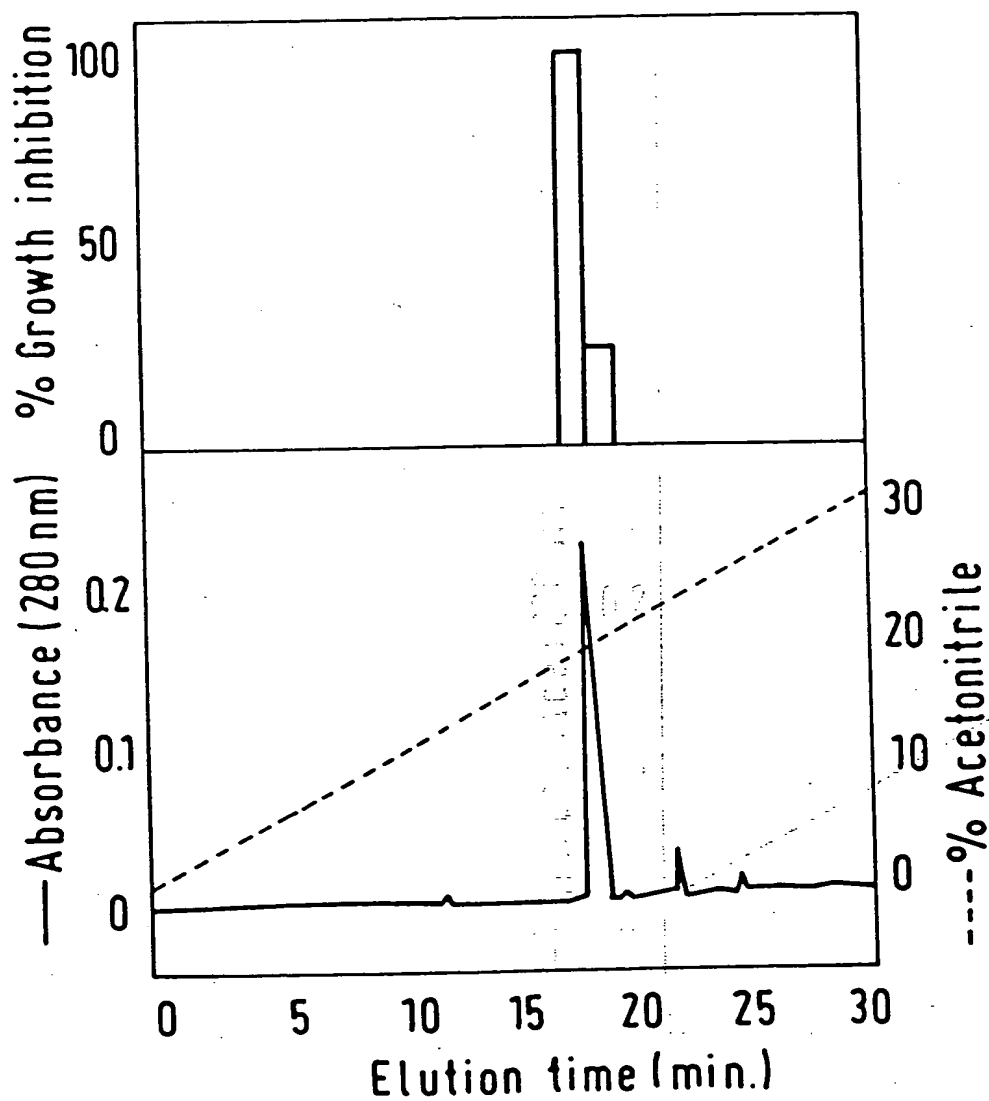


FIG. 16

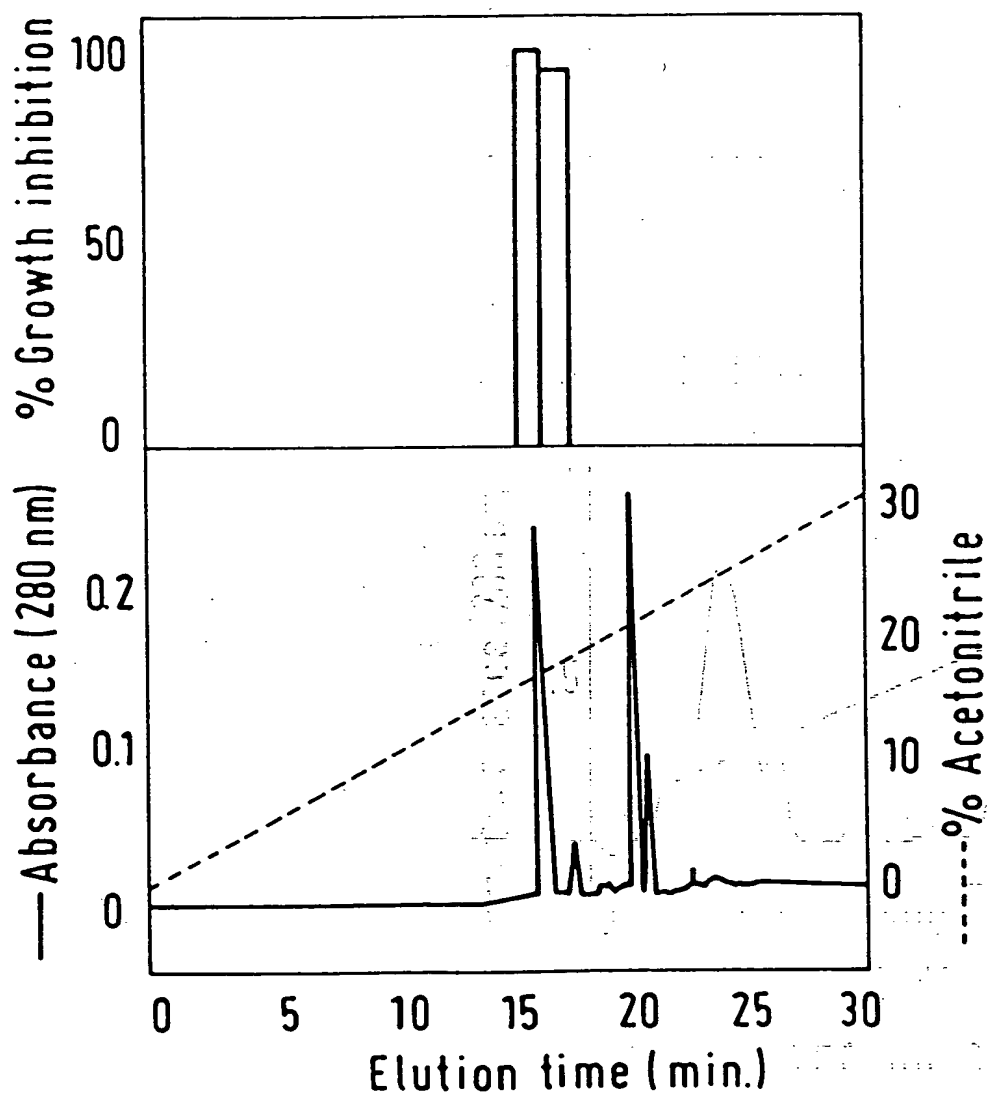


FIG. 17

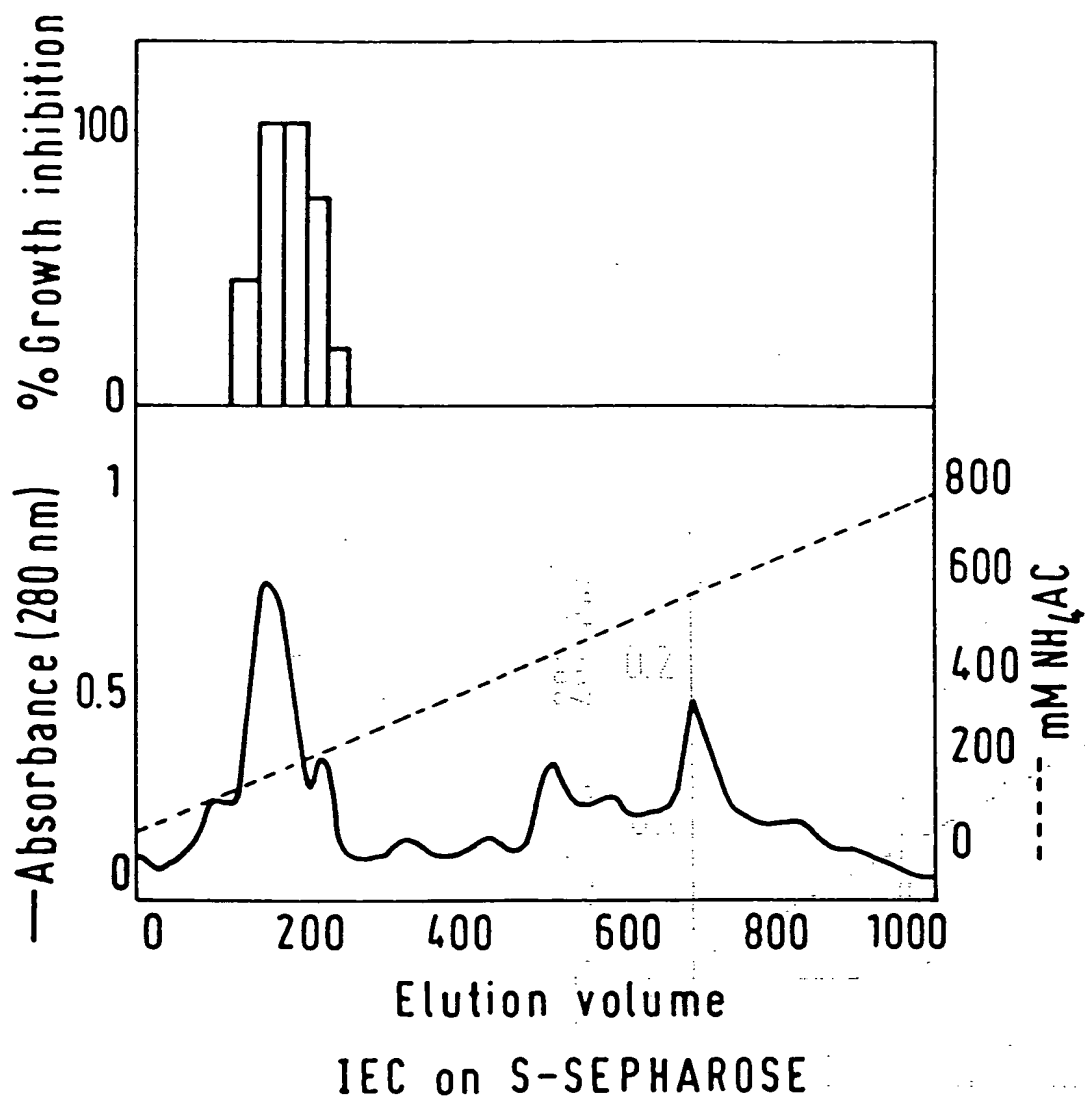


FIG. 18

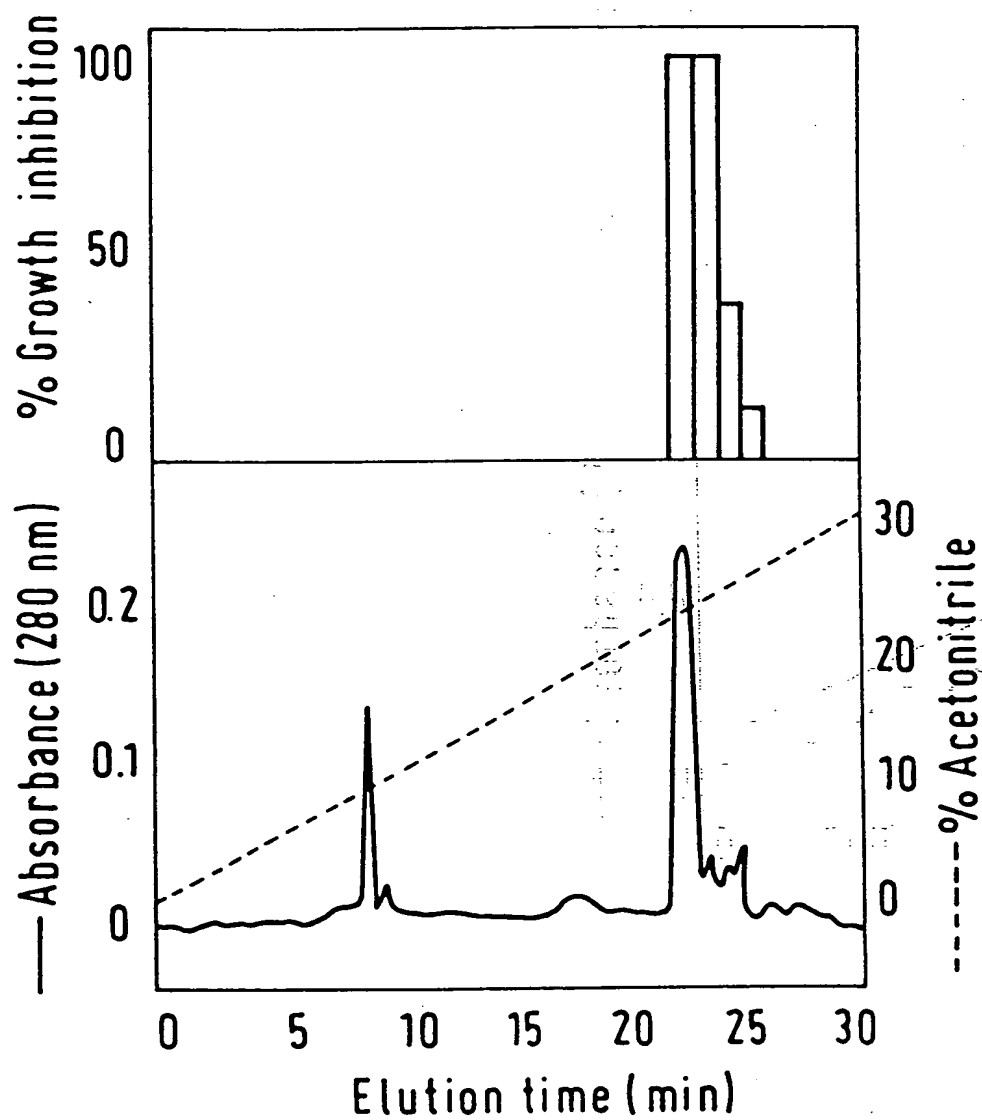


FIG. 19

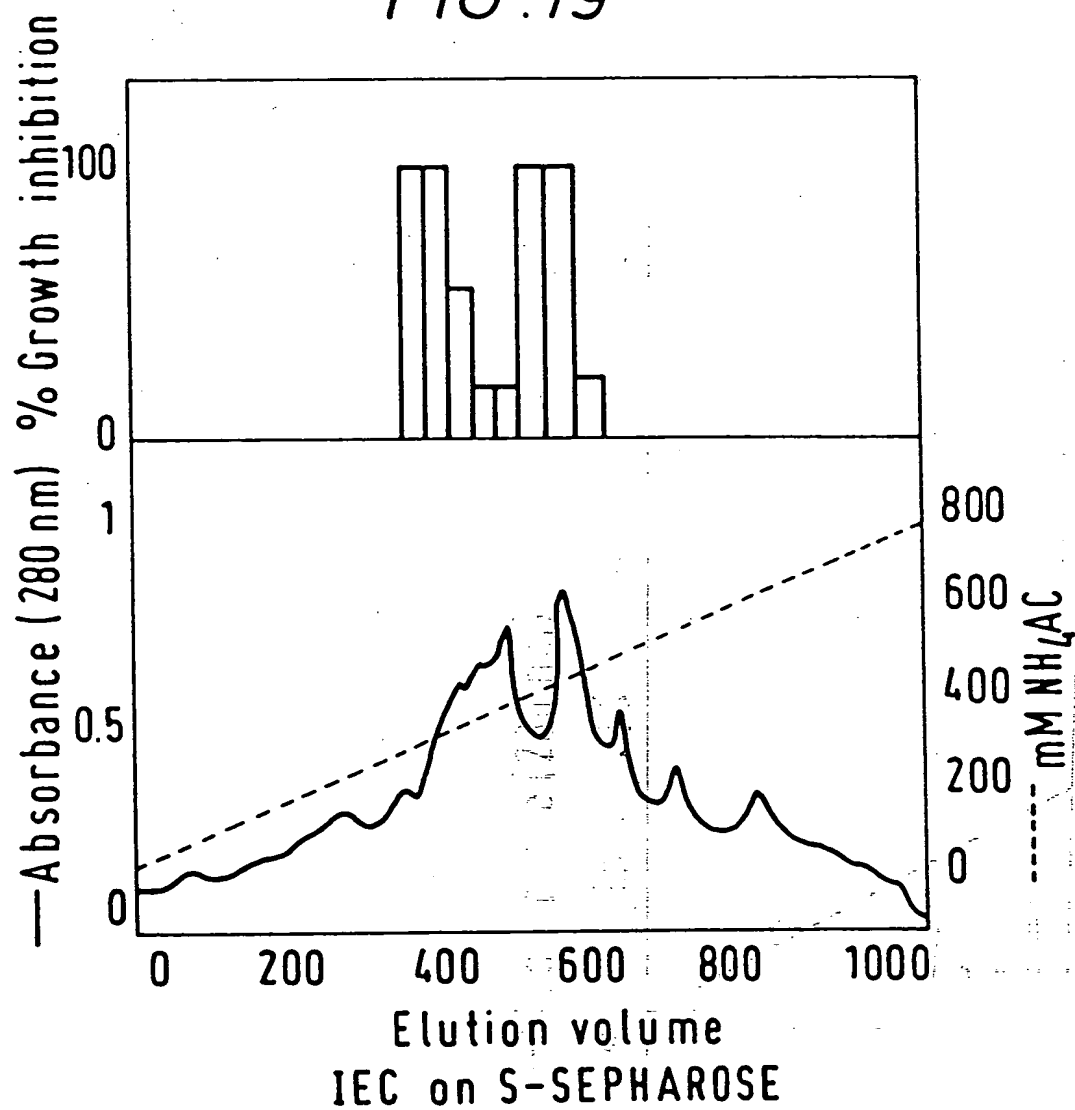


FIG. 20

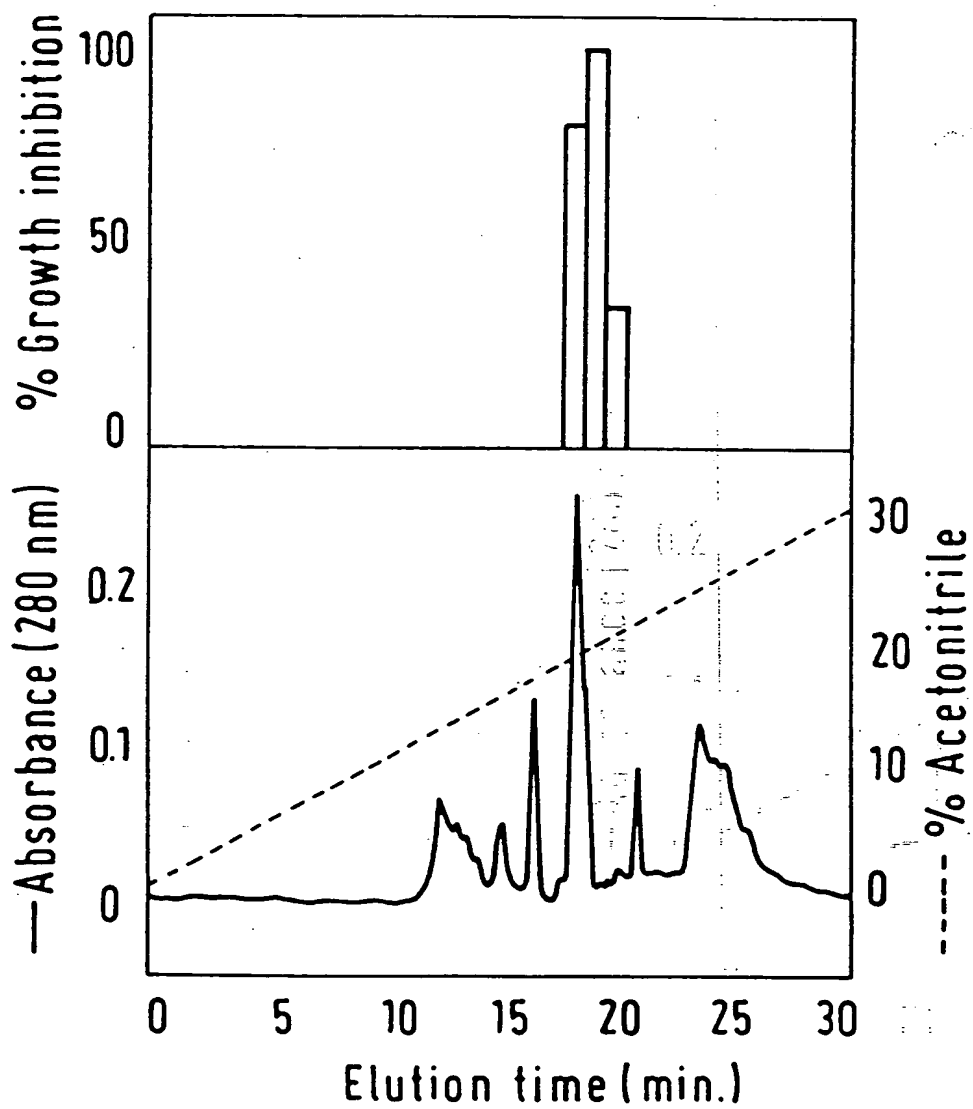


FIG. 21

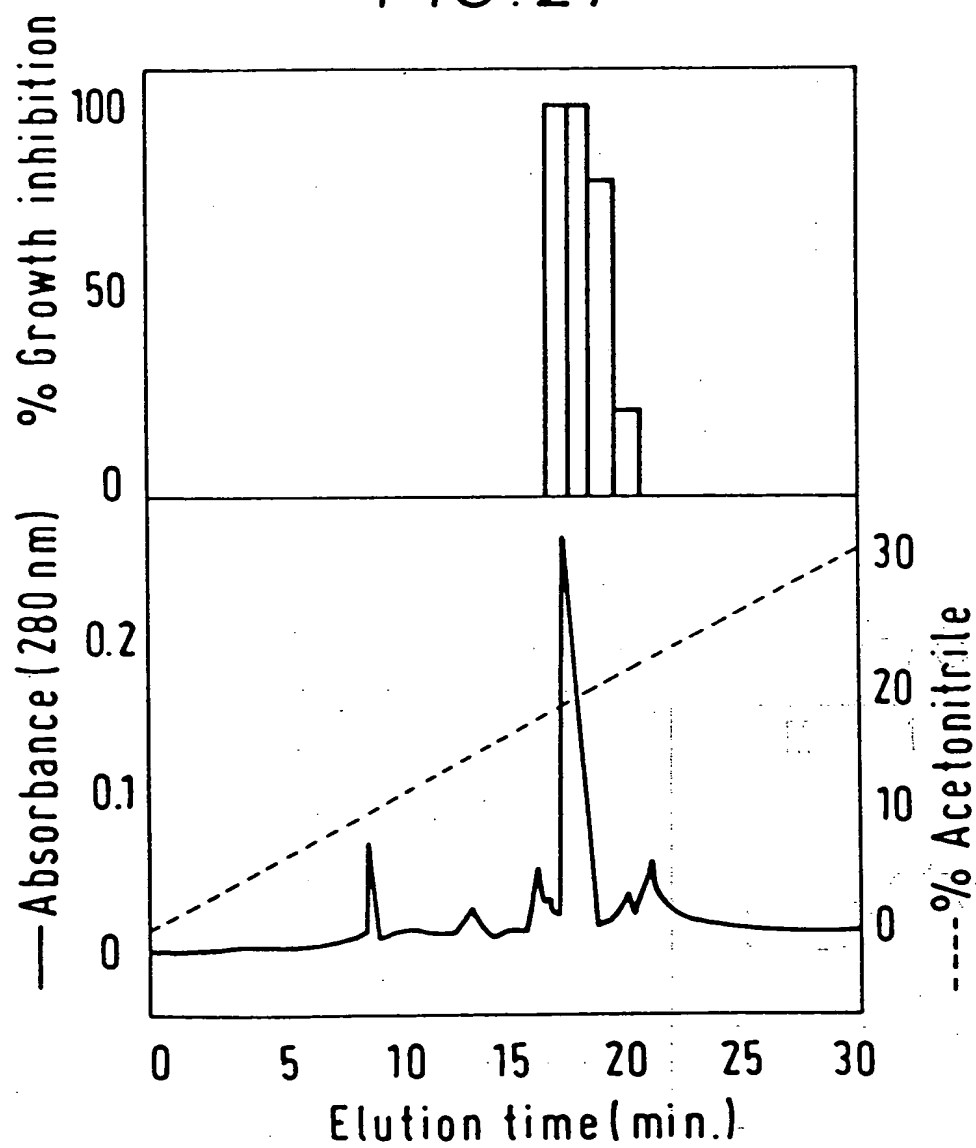


FIG. 22

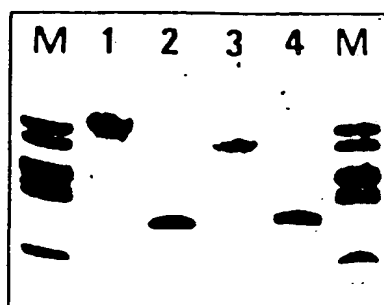


FIG. 23

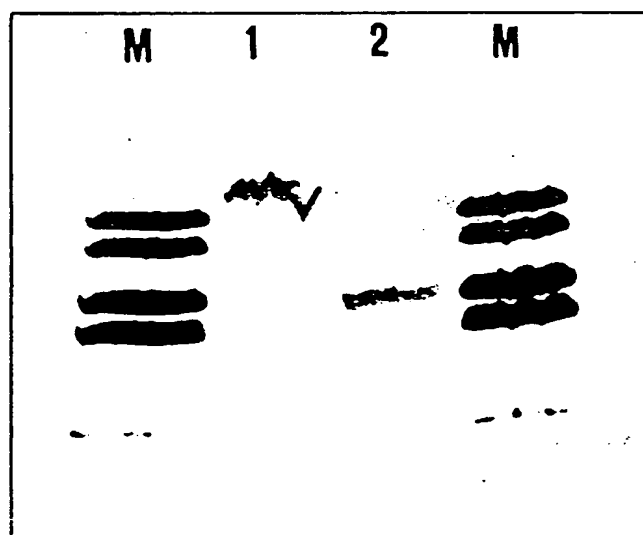


FIG. 24

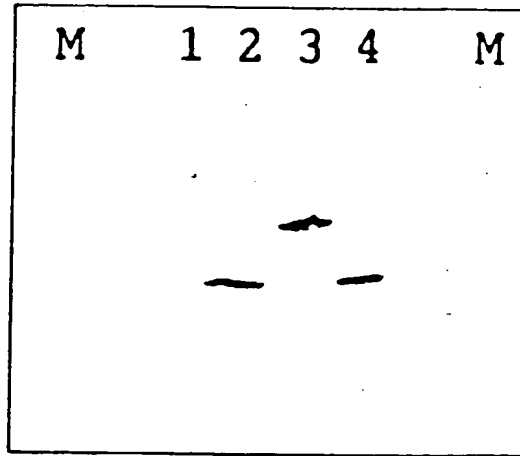


FIG. 25

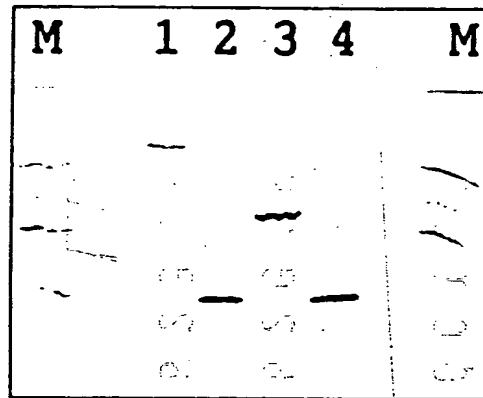


FIG. 26

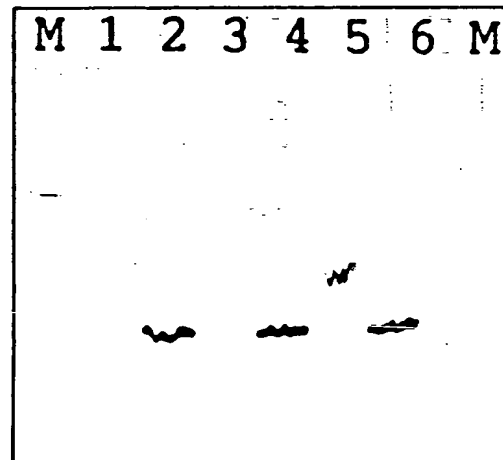


FIG. 27

Rs-AFP1 (Q) K L C E R P S G T W S G V C G N N

Rs-AFP2 (Q) K L C Q R P S G T W S G V C G N N

INACKNQCI NLEKARHGSCNYVFPAHK

INACKNQCI RLEKARHGSC

Br-AFP1

Br-AFP2 R

Bn-AFP1

Bn-AFP2

Sa-AFP1

Sa-AFP2 R ;

At-AFP1 S

FIG. 28

Dm-AMP1 E L C E K A S K T W S G N C G N T G H C D N

Dm-AMP2 E V C E K A S K T W S G N C G N T G H C

Cb-AMP1 E L C E K A S K T W S G N C G N T K H C D D

Cb-AMP2 E L C E K A S K T W S G N C G N T K H C D N

Q C K S W E G A A H G A C H V R N G K H M C F C Y F N C

Q C K S W E G A A H G A C H V R N G K H M C F C Y F N C

K C K S W E G A A H G A C H V R S G K H M C F C Y F N C

FIG. 29

LC-AFP K T C E N L S G T F K G P C I P D G N C N K H C K N

Ct-AMPI N L C E R A S L T W T G N C G N T G H C D T Q C R N

N E H L L S G R C R D D F ? - - C W C T R N C

W E S A K H G A C H K R G N W K C F C Y F D C

FIG. 30 (1/3)

Rs-AFP1 (Q)	K	L	C	E	R	P	S	G	T	W	S	G	V	C	G	N	N	A	C	
Dm-AMP1	E	L	C	E	K	A	S	K	T	W	S	G	N	C	G	N	T	G	H	C
Cb-AMP1	E	L	C	E	K	A	S	K	T	W	S	G	N	C	G	N	T	K	H	C
Cb-AMP2	E	L	C	E	K	A	S	K	T	W	S	G	N	C	G	N	T	K	H	C
Lc-AFP	K	T	C	E	N	L	S	G	T	F	K	G	P	C	I	P	D	G	N	C
Ct-AMP1	N	L	C	E	R	A	S	L	T	W	T	G	N	C	G	N	T	G	H	C
pI230	N	T	C	E	N	L	A	G	S	Y	K	G	V	C	F	G	G	-	-	C
pI39	N	T	C	E	H	L	A	D	T	Y	R	G	V	C	F	T	N	A	S	C
pSAS10	K	T	C	E	L	N	A	D	T	Y	R	G	P	C	F	T	T	G	S	C
pI322	R	H	C	E	S	L	S	H	R	F	K	G	P	C	T	R	D	S	N	C
SI α 2	R	V	C	M	G	K	S	A	G	F	K	G	L	C	M	R	D	Q	N	C
γ 1pur	K	I	C	R	R	R	S	A	G	F	K	G	P	C	M	S	N	K	N	C

00750504 011201

FIG. 30 (2/3)

K	N	Q	C	I	N	L	E	K	A	R	H	G	S	C	N	Y	V	F
D	N	Q	C	K	S	W	E	G	A	A	H	G	A	C	H	V	R	N
D	D	Q	C	K	S	W	E	G	A	A	H	G	A	C	H	V	R	N
D	N	K	C	K	S	W	E	G	A	A	H	G	A	C	H	V	R	S
N	K	H	C	K	N	N	E	H	L	L	S	G	R	C	R	D	D	F
D	T	Q	C	R	N	W	E	S	A	K	H	G	A	C	H	K	R	-
D	R	H	C	R	T	Q	E	G	A	I	S	G	R	C	R	D	D	F
D	D	H	C	K	N	K	A	H	L	I	S	G	T	C	H	-	D	W
D	D	H	C	K	N	K	E	H	L	L	S	G	R	C	R	-	D	D
A	S	V	C	E	T	-	E	R	F	S	G	G	N	C	H	-	G	F
A	Q	V	C	L	-	Q	E	G	W	G	G	G	N	C	D	G	V	M
A	Q	V	C	Q	-	Q	E	G	W	G	G	G	N	C	D	G	P	F

00750584 011201

FIG. 30 (3/3)

P	A	H	K	C	I	C	Y	F	P	C
G	K	H	M	C	F	C	Y	F	N	C
G	K	H	M	C	F	C	Y	F	N	C
G	K	H	M	C	F	C	Y	F	N	C
-	-	-	?	C	W	C	T	R	N	C
G	N	W	K	C	F	C	Y	F	D	C
-	-	-	R	C	W	C	T	K	N	C
-	-	-	K	C	F	C	T	Q	N	C
-	-	V	R	C	W	C	T	R	N	C
-	R	R	R	C	F	C	T	K	P	C
-	-	R	Q	C	K	C	I	R	Q	C
-	-	R	R	C	K	C	I	R	Q	C

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FIG. 31A(1/2)

Dm-AMP1	GAG CTT TGC GAG AAG GCT TCT AAG ACT TGG TCT GGA AAC
	TGG GAG GGA GCT GCT CAT GGA GCT TGC CAT GTT AGA AAC
Dm-AMP2	GAG GTT TGC GAG AAG GCT TCT AAG ACT TGG TCT GGA AAC
Cb-AMP1	GAG CTT TGC GAG AAG GCT TCT AAG ACT TGG TCT GGA AAC
	TGG GAG GGA GCT GCT CAT GGA GCT TGC CAT GTT AGA AAC
Cb-AMP2	GAG CTT TGC GAG AAG GCT TCT AAG ACT TGG TCT GGA AAC
	TGG GAG GGA GCT GCT CAT GGA GCT TGC CAT GTT AGA TCT

FIG. 31A (2/2)

TGC GGA AAC ACT GGA CAT TGC GAT AAC CAA TGC AAG TCT

GGA AAG CAT ATG TGC TTC TGC TAC TTC AAC TGC

TGC GGA AAC ACT GGA CAT TGC

TGC GGA AAC ACT AAG CAT TGC GAT GAT CAA TGC AAG TCT

GGA AAG CAT ATG TGC TTC TGC TAC TTC AAC TGC

TGC GGA AAC ACT AAG CAT TGC GAT AAC AAG TGC AAG TCT

GGA AAG CAT ATG TGC TTC TGC TAC TTC AAC TGC

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10021040505260

FIG. 31B

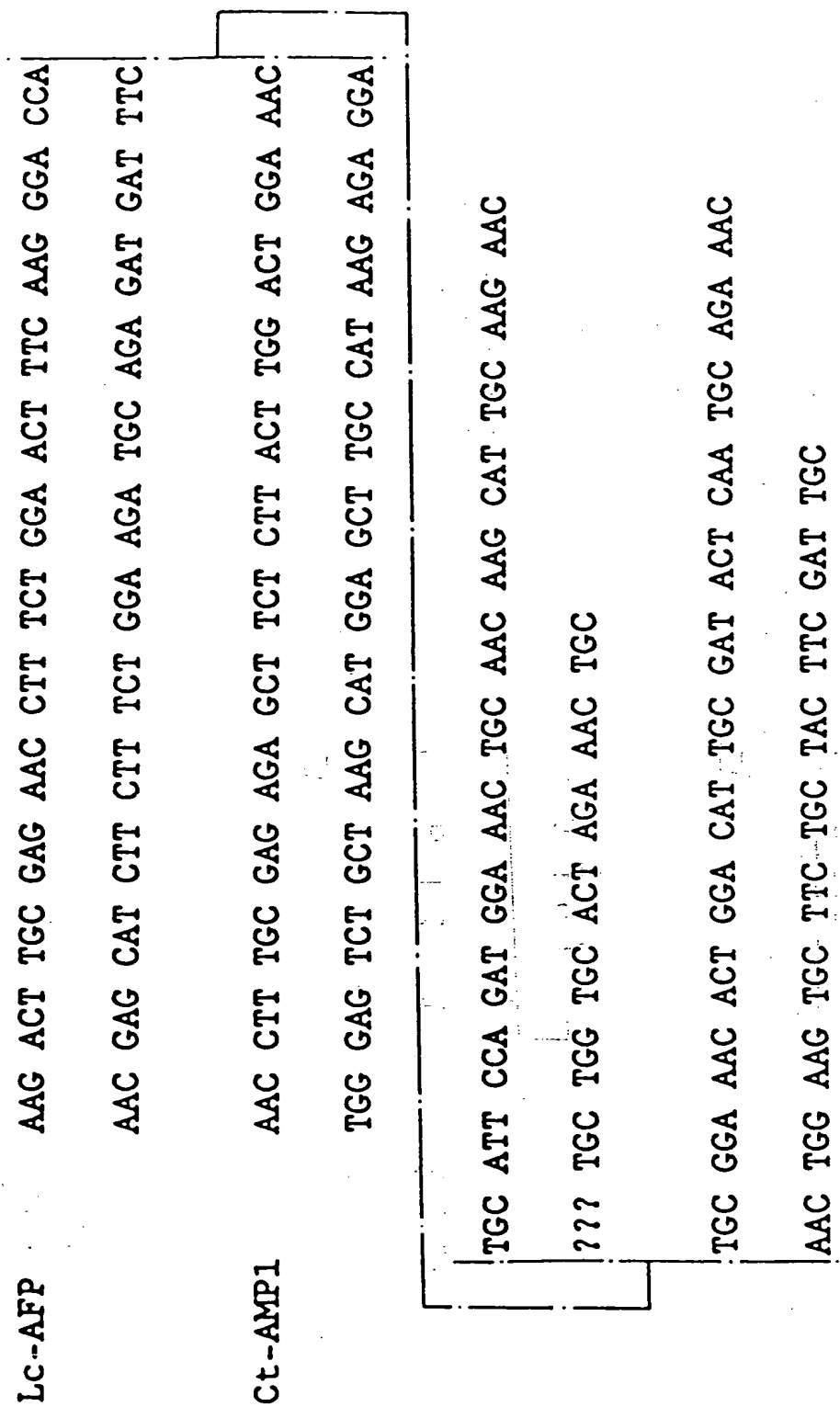


FIG. 32

Rs-nsLTP

A L S C G T V N S N L A A C I G Y L T Q

N A P L A R G C C T G V T N L N N M A ? T T P

FIG. 33 (1/2)

Rs-nsLTP

A L S C G T V N S N L A A C I G Y L T Q

So-nsLTP

G I T C G M V S S K L A P C I G Y L K G

Rc-nsLTP

V D C G Q V N S S L A S C I P F L T G

Dc-nsLTP

V L T C G Q V T G A L A P C L G Y L R S

Hv-nsLTP

A L N C G Q V D S K N K P C L T Y V Q G

Zm-nsLTP

A I S C G Q V A S A I A P C I S Y A R G

FIG. 33 (2/2)

N - A - - -	P L A R G C C T G V T N L N M A ?	T T P
G - - - -	P L G G S S G G I K A L N A A A A T T P	...
G V A S - -	P S A S - C C A G V Q N L K T L A P T S A	...
Q V N V P V P L T - -	C C N V V R G L N N A A R T T L	...
G P G - G - P S G L -	C C N G V R D L H N Q A Q S S G	...
Q - G S G - P S A - G	C C S G V R S L N N A A R T T A	...

FIG. 34

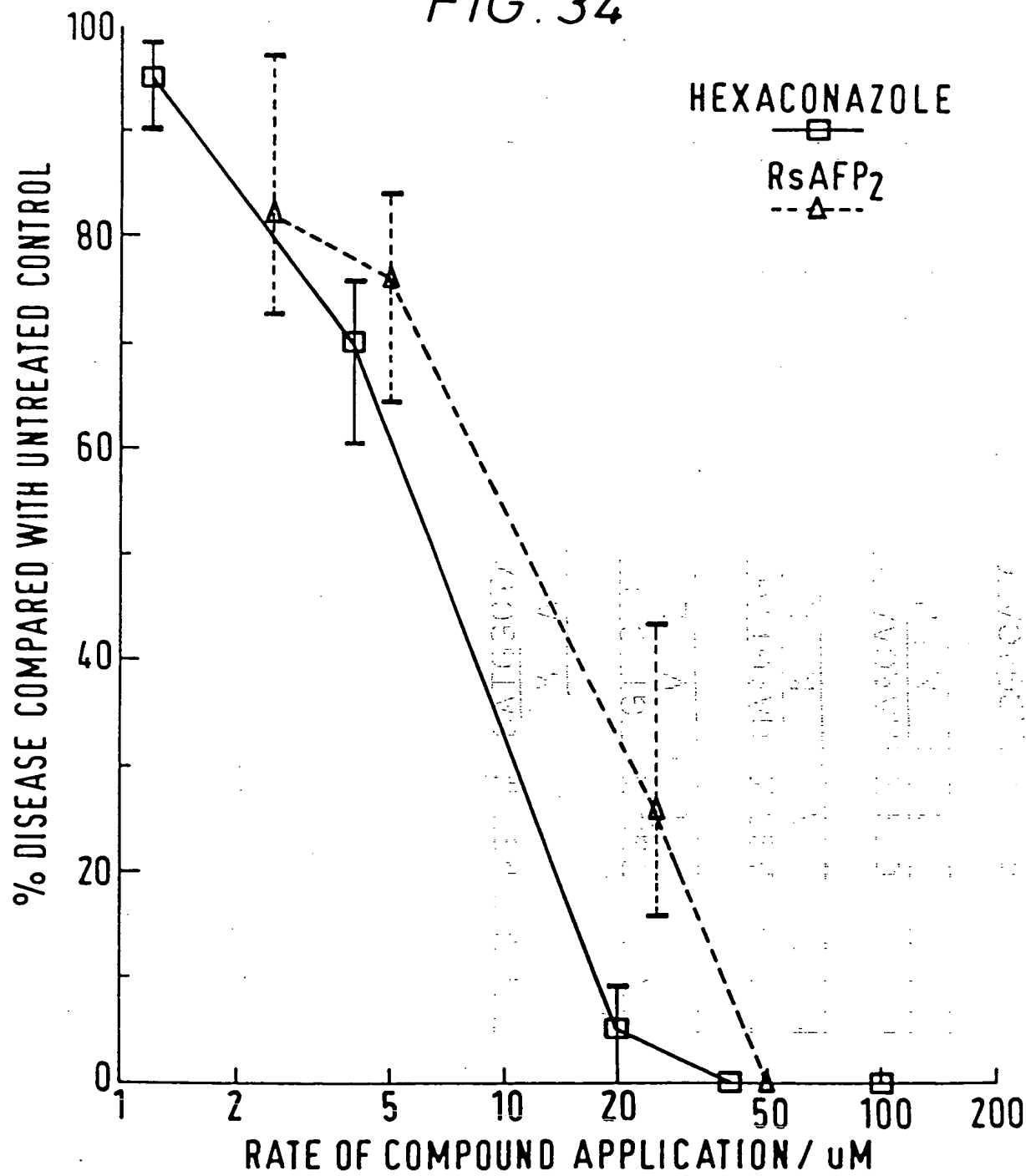


FIG. 35

GTTTATTAGTATCATGGCTAAGTTTGGTGTCATCATCGCACTT 45
M A K F A S I I A L

CTTTTGGCTGCTCTTGTTCTTTTGGCTGCTTTTCGAAGCACCAACA 90
L F A A L V L F A A F E A E T

ATGGTGGAAGCACAGAAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
M V E A Q K L C E R P S G T W

TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
S G V C G N N N A C K N Q C I

AACCTTGAGAAAGCACGACATGGATCTTGCACACTATGTCTTCCCA 225
N L E K A R H G S C N Y V F P

GCTCACAAGTGTATCTGCTACTTTCCTTGTIAATTATCGCAAAC 270
A H K C I C Y F P C *

TCTTTGGTGAATAGTTTTTATGTAATTTACACAAATAAGTCAGT 315

GTCACATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT 360

GTTGGTTCGGTTATACAAATAAAGTTTTTATTCACCAAAAAAAA 405

AAAAAAA 414

FIG. 36

GGAAATAACGCATGCAAGAAATCAGTGCAATTCGACTTGAGAAA	45
G N N A C K N Q C I R L E K	
GCACGACATGGGTCTTGCAACTATGTCTTCCCAGCTCACAAGTGT	90
A R H G S C N Y V F P A H K C	
ATCTGTTATTTCCCTTGTIAA <u>TTCCATAAACTC</u> TTCCGGTGGTTAA	135
I C Y F P C *	
TAGTGCGGCATATTACATATAATTAATAAGTTTGTCACACTATT	180
TATTAGTGACTTTATGACATGTGCCAGGTATGTTTATGTTGGGTT	225
GGTGTAAATAAAAAAGTTCACGGATAATAAGATGATAAGCTCA	270
CGTCGCCAAAAAA	284

FIG. 37 (1/2)

CCCCGGGCTGCAG

GAATTCGGGGCCGC

10 20 30 40 50 60
 | | | | |
 GTTTATTAGTCATCGGCTAAGTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTT

M A K F A S I I A L L F A A L

70 80 90 100 110 120
 | | | | |
 GTTCTTTTGCTGCTTTTCGAAGCACCAACAATGGTGAAGCACAGAAAGTTGTGCCAAAGG

V L F A A F E A P T M V E A Q K L C Q R

FIG. 37 (2/2)

130 | 140 | 150 | 160 | 170 | 180 |
 CCAAGTGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT

P	S	G	T	W	S	G	V	C	G	N	N	A	C	K	N	Q	C	I
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

190 | 200 | 210 | 220 | 230 | 240 |
 AGACTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCAGCTCACAAAGTGTATC

R	L	E	K	A	R	H	G	S	C	N	Y	V	F	P	A	H	K	C	I
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

250 | 260 |
 TGCTACTTCCCTTGTTAATAG

C	Y	F	P	C
---	---	---	---	---

- - 55537

FIG. 38

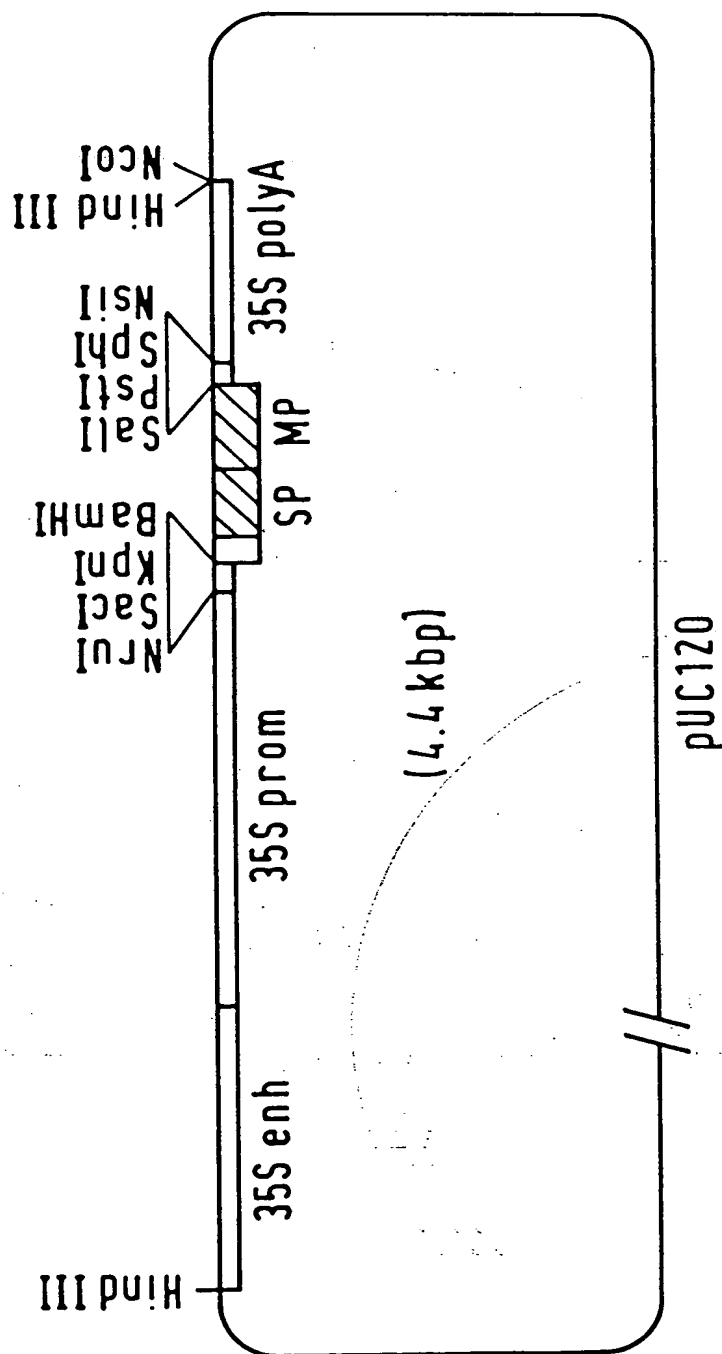


FIG. 39

